

***In the Claims***

Please amend and add the following claims according to the following listing of claims under 37 CFR 1.121.

**Listing of Claims under 37 CFR 1.121 (revised):**

1-5 (CANCELED)

6. (NEW): A process for identifying one or more bi-allelic markers linked to a bi-allelic trait-causing polymorphism in a species of creatures, comprising the acts of:

- a) choosing two or more bi-allelic covering markers so that a CL-F region is systematically covered by the two or more covering markers, the CL-F region being a collection of one or more points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency;
- b) choosing a statistical linkage test based on allelic association for each covering marker;
- c) choosing a sample of individuals for each covering marker ;
- d) obtaining genotype data/sample allele frequency data for each covering marker and the sample chosen for each covering marker, and obtaining phenotype status data for the trait for each individual in the sample chosen for each covering marker;
- e) calculating evidence for linkage between each covering marker and the trait-causing polymorphism using the statistical linkage test based on allelic association chosen for each covering marker and the genotype data/sample allele frequency data for each covering marker and using the phenotype status data for the trait for each individual in the sample chosen for each covering marker obtained in d); and
- f) identifying those covering markers as linked to the trait-causing polymorphism which show evidence for linkage based on the calculations of e).

7. (NEW): A process as in claim 6, wherein the CL-F region is for a species and a population and the population is a group of individuals as in the field of population genetics, wherein the CL-F region is N covered to within [x, y] by the two or more bi-allelic covering markers, wherein x is less than or equal to about  $D_{CL}$  or the equivalent thereof and y is less than or equal to about 0.2,  $D_{CL}$  is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1, wherein the choice of covering markers is not based on the assumption that a covering marker is the trait-causing polymorphism, wherein the group of two or more covering markers is not an essentially one-dimensional panel of markers for a linkage study, wherein the essentially one-dimensional panel is a panel not based on using similarity of marker allele frequency and possible trait-causing polymorphism allele frequency to increase the power of an association-based linkage test to detect evidence for linkage.

8. (NEW): A process as in claim 7, wherein the CL-F region is a segment-subrange.

9. (NEW): A process as in claim 6, wherein the CL-F region is for a species and a population and the population is a group of individuals as in the field of population genetics, wherein the choice of covering markers is not based on the assumption that a covering marker is the trait-causing polymorphism, wherein the group of covering markers are not an essentially one-dimensional panel of markers for a linkage study, wherein the essentially one-dimensional panel is a panel not based on using similarity of marker allele frequency and possible trait-causing polymorphism allele frequency to increase the power of an association-based linkage test to detect evidence for linkage, wherein a chromosome or a chromosomal subregion of interest is completely covered by chromosomal segments, wherein the segments may or may not overlap, wherein the segments are short enough that polymorphisms within each segment are likely to be in linkage disequilibrium with each other, wherein each covering marker belongs to a subset of covering markers, wherein there is more than one marker in each subset, whereby there are two or more markers in each subset, wherein the markers in each subset have approximately the same allele frequencies, wherein the difference between the least common allele frequencies of any two markers in a subset does not exceed 0.15, wherein the markers in each subset are located within one segment and within each segment there are five subsets, or more or less than five subsets of covering markers, wherein the approximate allele frequencies of the markers in each subset are spaced approximately evenly over a subrange.

10. (NEW): A process as in claim 9, wherein no two covering markers in the same subset provide nearly identical information with respect to their linkage and association with a third polymorphism, wherein the chromosomal location coordinates of the CL-F region range over the chromosome or the subregion of interest and the least common allele frequency coordinates range over the subrange, whereby each CL-F point located on the chromosome or in the subregion of interest and within the subrange is in the CL-F region, whereby the CL-F region is a rectangular region bounded by the chromosome or subregion of interest in the chromosomal location dimension and bounded by the subrange in the allele frequency dimension, wherein each point in the CL-F region is N-covered to within [L, y] by markers belonging to a subset, whereby each point in the CL-F region has the characteristic described in (1): (1) any one CL-F point is N-covered to within [L, y] by covering markers that belong to a segment that contains the point, L is the length of the segment, y is any number greater than or equal to 0.15, and N ≥ 2.

11. (NEW): A process as in claim 10, wherein the species is human being.

12. (NEW): A process as in claim 10, wherein the least common allele frequency coordinates of the CL-F region range over the subrange, and the subrange is the subrange 0 to less than 0.1.

13. (NEW): A process as in claim 10, wherein N > 2.

14. (NEW): A process as in claim 10, wherein the process uses thousands of bi-allelic covering markers.

15. (NEW): A process as in claim 6, further comprising the act of:

f)localizing the trait-causing polymorphism to the chromosomal location-least common allele frequency (CL-F) location of one or more markers that show evidence for linkage based on the calculations of act e), wherein the localizing uses a technique or techniques that detects gradients, wherein the detection technique or techniques uses a gradient along the allele frequency dimension.

16. (NEW): One or more copies of a set of oligonucleotides, the set of oligonucleotides being complementary to a group of two or more bi-allelic covering markers of the same species, wherein the group of covering markers systematically cover a CL-F region, the CL-F region being a collection of one or more points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency.

17. (NEW): One or more copies of a set of oligonucleotides as in claim 16, wherein the CL-F region is for a species and a population and the population is a group of individuals as in the field of population genetics, wherein the CL-F region is N covered to within [x, y] by the two or more bi-allelic covering markers, wherein x is less than or equal to about  $D_{CL}$  or the equivalent thereof and y is less than or equal to about 0.2,  $D_{CL}$  is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1, wherein the choice of covering markers is not based on the assumption that a covering marker is the trait-causing polymorphism, wherein the group of two or more covering markers is not an essentially one-dimensional panel of markers for a linkage study, wherein the essentially one-dimensional panel is a panel not based on using similarity of marker allele frequency and possible trait-causing polymorphism allele frequency to increase the power of an association-based linkage test to detect evidence for linkage.

18. (NEW): One or more copies of a set of oligonucleotides as in claim 17, wherein the CL-F region is a segment-subrange.

19. (NEW): One or more copies of a set of oligonucleotides as in claim 16, wherein the CL-F region is for a species and a population and the population is a group of individuals as in the field of population genetics, wherein the choice of covering markers is not based on the assumption that a covering marker is the trait-causing polymorphism, wherein the group of covering markers are not an essentially one-dimensional panel of markers for a linkage study, wherein the essentially one-dimensional panel is a panel not based on using similarity of marker allele frequency and possible trait-causing polymorphism allele frequency to increase the power of an association-based linkage test to detect evidence for linkage, wherein a chromosome or a chromosomal subregion of interest is completely covered by chromosomal segments, wherein the segments may or may not overlap, wherein the segments are short enough that polymorphisms within each segment are likely to be in linkage disequilibrium with each other, wherein each covering marker belongs to a subset of covering markers, wherein there is more than one marker in each subset, whereby there are two or more markers in each subset, wherein the markers in each subset have approximately the same allele frequencies, wherein the difference between the least common allele frequencies of any two markers in a subset does not exceed 0.15, wherein the markers in each subset are located within one segment and within each segment there are five subsets, or more or less than five subsets of covering markers, wherein the approximate allele frequencies of the markers in each subset are spaced approximately evenly over a subrange.

20. (NEW): One or more copies of a set of oligonucleotides as in claim 19, wherein no two covering markers in the same subset provide nearly identical information with respect to their linkage and association with a third polymorphism, wherein the chromosomal location coordinates of the CL-F region range over the chromosome or the subregion of interest and the least common allele frequency coordinates range over the subrange, whereby each CL-F point located on the chromosome or in the subregion of interest and within the subrange is in the CL-F region, whereby the CL-F region is a rectangular region bounded by the chromosome or subregion of interest in the chromosomal location dimension and bounded by the subrange in the allele frequency dimension, wherein each point in the CL-F region is N-covered to within [L, y] by markers belonging to a subset, whereby each point in the CL-F region has the characteristic described in (1): (1) any one CL-F point is N-covered to within [L, y] by covering markers that belong to a segment that contains the point, L is the length of the segment, y is any number greater than or equal to 0.15, and  $N \geq 2$ .

21. (NEW): One or more copies of a set of oligonucleotides as in claim 20, wherein the species is human being.

22. (NEW): One or more copies of a set of oligonucleotides as in claim 20, wherein the least common allele frequency coordinates of the CL-F region range over the subrange, and the subrange is the subrange 0 to less than 0.1.

23. (NEW): One or more copies of a set of oligonucleotides in claim 20, wherein  $N > 2$ .

24. (NEW): One or more copies of a set of oligonucleotides as in claim 20, wherein the process uses thousands of bi-allelic covering markers.